

FIG. 1A

gtgttgcctcc actgtcagtc ctccagagcc tcaagagatc tttggccat atcagcttc 60
 tttccaaaat gaacacaccc aggggcagga aagaatgctc tttccttggt cattaagggg 120
 cctggagtc ctggaccagc tttcatgca gctagaccac ttacatgcaa ctagagcctt 180
 gactttgaaa cgaaggacaa aagcatctct tgctaaaggt aacttctgct gcttagaacc 240
 cagcctcctc accaccatct gatctatctt gttctttca caaaaggctc tgaagacatc 300
 atg aac cca caa cgg gag gca gca ccc aaa tcc tat gct att cgt gat 348
 Met Asn Pro Gln Arg Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp
 1 5 10 15
 tct cga cag atg gtg tgg gtc ctg agt gga aat tct tta ata gca gct 396
 Ser Arg Gln Met Val Trp Val Leu Ser Gly Asn Ser Leu Ile Ala Ala
 20 25 30
 cct ctt agc cgc agc att aag cct gtc act ctt cat tta ata gcc tgt 444
 Pro Leu Ser Arg Ser Ile Lys Pro Val Thr Leu His Leu Ile Ala Cys
 35 40 45
 aga gac aca gaa ttc agt gac aag gaa aag ggt aat atg gtt tac ctg 492
 Arg Asp Thr Glu Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu
 50 55 60
 gga atc aag gga aaa gat ctc tgt ctc ttc tgt gca gaa att cag ggc 540
 Gly Ile Lys Gly Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly
 65 70 75 80
 aag cct act ttg cag ctt aag gaa aaa aat atc atg gac ctg tat gtg 588
 Lys Pro Thr Leu Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val
 85 90 95
 gag aag aaa gca cag aag ccc ttt ctc ttt ttc cac aat aaa gaa ggc 636
 Glu Lys Lys Ala Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly
 100 105 110
 tcc act tct gtc ttt cag tca gtc tct tac cct ggc tgg ttc ata gcc 684
 Ser Thr Ser Val Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala
 115 120 125
 acc tcc acc aca tca gga cag ccc atc ttt ctc acc aag gag aga ggc 732
 Thr Ser Thr Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly
 130 135 140
 ata act aat aac act aac ttc tac tta gat tct gtg gaa taa 774
 Ile Thr Asn Asn Thr Asn Phe Tyr Leu Asp Ser Val Glu
 145 150 155
 atccagccata ggctgtgggt ggctggttcc aggatagaga atcaagctgt cagagtcatc 834
 ttaacagatc attatgcgac tgagttcaact agcagttcag cccatccata gcttacctca 894

FIG. 1B

ttcttactat ccaaaagcca ctccttcctc caaacatcca ttctgttacc aagaccctca 954
ctcgaatgtc actatccaa gatgaaacct aaaaatcact ttccattctt tcttgatctt 1014
accccaccat ccactcagct gccatgccc a gtttagttaa ccccccaat gctgcttc 1074
gcaaccttcc attccttattc ctttgccaa cccatgatgt agagatgtgg attcatgaca 1134
ttttgttcat acaacttctt caataaaaca ttataatatg tgcccaaaag ataaagctga 1194
agaatgagat gaatgtgaaa taaaaggaaa gcatgtcttc ctaatcctaa 1244

FIG. 2

1	50
IL-1_delta ~~~~~ ~~~~~ ~~~~~ ~~~~~ MNPQ REAAPKSYAI RDSRQMVWVL	
IL-1ra-L ~~~~~ ~~~~~ ~~~~~ MNPQ REAAPKSYAI RDSRQMVWVL	
IL-1_epsilon ~~~~~ ~~~~~ ~~~~~ MEKAL KIDTPQQGSI QDINHRVWVL	
IL-1ra_sec MEICRGLRSH LITLLLFLFH SETICRPSGR KSSKMQAFRI WDVNQKTFYL	
IL-1_beta ~~~~~ ~~~~~ ~~~~~ APVRSLNCTL RDSQQKSLVM	
consensus ----- MNPQ -EAAP-SYAI RDS-Q-VWVL	
51	
IL-1_delta SG.NSLIAAP LSRSIKPVTL HLIACRDTEF SDKEKGKGNMVTY LGIKGKDLCL	100
IL-1ra-L SG.NSLIAAP LSRSIKPVTL HLIACRDTEF SDKEKGKGNMVTY LGIKGKDLCL	
IL-1_epsilon QD.QTLLIAVP RKDRMSPVTI ALISCRHVET LEKDRGNPIY LGLNGLNLCL	
IL-1ra_sec RN.NQLVAGY LQ...GP.NV NLEEKIDVVP IEP...HALF LGIHGGKMCL	
IL-1_beta SGPYELKALH LQGQDMEQQV .VFSMSFVQG EESNDKIPVA LGLKEKNLYL	
consensus SG-NSLIAAP L-RSIKPVT- HLI-CRDVEF SEKEKGN-VY LGIKGK-LCL	
101	
IL-1_delta FCAEIQGKPT LQLKLQGSQD .NIGKDTCWK LVGIHTCINL DVRESCFMG.	150
IL-1ra-LFCAEIQGKPT LQLKEKNIMD LYVEKKAQKP FLFFH...NK EGSTSVFQSV	
IL-1_epsilon MCAKVGQDQPT LQLKEKDIMD LYNQPEPVKS FLFYH...SQ SGRNSTFESV	
IL-1ra_sec SCVKSGDETR LQLEAVNITD LSENRKQDKR FAFIR...SD SGPTTSFESA	
IL-1_beta SCVLKDDKPT LQLESVDPKN .YPKKKMEKR FVFNKIEINN KLE...FESA	
consensus -CA-I-DKPT LQLKE--IMD LY--KK--KR F-FIH--IN- SGRTS-FES-	
151	
IL-1_delta TLDQWGIGVG RKKWKSSFQH HHLRKKDKDF SSMRTNIGMP GRM	193
IL-1ra-L SYPGWFIATS TTSGQPIF... .LTKERGI TN.NTNFYLD SVE	
IL-1_epsilon AFPGWFIAVS SEGGCPLILT QELGKANTTD FGLTMLF~~~ ~~	
IL-1ra_sec ACPGWFLCTA MEADQPVSLT N...MPDEGV MVTKFYFQED E~~	
IL-1_beta QFPNWYISTS QAENMPVFLG GTKGGQDITD FTMQFVSS~~ ~~	
consensus AFPGWFIATS -E-GQPVFLT --LGKKD--D F-M--NF--D ---	